

Input file Fbhl8903FL.seq; Output File 18903.trans
Sequence length 1983

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CCTTTAGCCAATTCGGCCGAGGCCTCCCGCCCACTACTTGCTGGCAGGGATTAAGAGCAGATAAAAGTGCTGCTCACAC
      M P S T V L P S T V L P S L L      15
ACTGTAGACACGGCTACC ATG CCA TCC ACA GTG TTG CCA TCC ACA GTG TTG CCA TCA CTC CTG      45

P T A G A G W S M R W I L C W S L T L C      35
CCC ACA GCA GGA GCT GGC TGG AGC ATG AGG TGG ATT CTG TGC TGG AGC CTC ACC CTC TGC      105

L M A Q T A L G A L H T K R P Q V V T K K      55
CTG ATG GCG CAG ACG GCC TTG GGT GCC TTG CAC ACC AAG AGG CCT CAA GTG GTC ACC AAA      165

Y G T L Q G K Q M H V G K T P I Q V F L      75
TAT GGA ACC CTG CAA GGA AAA CAG ATG CAT GTG GGG AAG ACA CCC ATC CAA GTC TTT TTA      225

G V P F S R P P L G I L R F A P P E P P      95
GSA GTC CCC TTC TCC AGA CCT CCT CTA GGT ATC CTC AGG TTT GCA CCT CCA GAA CCC CC      285

P W K G I R D A T T Y P P G C L Q E C S      115
GAG CCC TGG AAA GGA ATC AGA GAT GCT ACC ACC TAC CCG CCT GGG TGC CTG CAG GAG TCC      345

G Q L A S M Y V S T R E R Y K W L R F      135
GAG GGC CAG CTG GCC TCG ATG TAC GTC AGC ACG CGG GAA CGS TAC AAG TGG CTG CGC TTC      405

S E D C L Y L N V Y A P A R A P G D P Q      155
AGC GAG GAC TGT CTG TAC CAG ATC GGC TAC GCG CGC GCG CCC GGG GAT CCC CAG      465

L P V M V W F P G G A F I V G A A S S Y      175
GAG CCA GTG ATG GTC TGG TTC CCG GGA GGC GCC TTC ATC GTG GGC GCT GCT TCT TCG TAC      525

G S D L A A R E K V V L V F L Q H R L      195
GAG GGC TCT GAC TTG GCC GCC CGC GAG AAA GTG GTG CTG GTG TTT CTG CAG CAC AGG CTC      585

G I F G F L S T D D S H A R G G N W G L L      215
GGC ATC TTC GGC TTC CTG AGC ACG GAC GAC AGC CAC GCG CGC GAG AAC TGG GGG CTG CTG      645

D Q M A A L R W V Q E N I A A F G G D P      235
GAC CAG ATG GCG GCT CTG CGC TGG GTG CAG GAG AAC ATC GCA GCC TTC GGG GGA GAC CCA      705

G N V T L F G Q S A G A M S I S G L M M      255
GGA AAT GTG ACC CTG TTC GGC CAG TCG GCG GGC ACC ATG AGC ATC TCA GGA CTG ATG ATG      765

S P L A S G L F H R A I S Q S G T A L F      275
TCA CCC CTA GCC TCG GGT CTC TTC CAT CGG GCC ATT TCC CAG AGT GGC ACC GCG TTA TTC      825

R L F I T S N P L K V A K K V A H L A G      295
AGA CTT TTC ATC ACT AGT AAC CCA CTG AAA GTG GCC AAG AAG GTT GCC CAC CTG GCT GGA      885

C N H N S T Q I L V N C L R A L S G T K      315
TGC AAC CAC AAC AGC ACA CAG ATC CTG GTA AAC TGC CTG AGG GCA CTA TCA GGG ACC AAG      945

V M R V S N K M R F L Q L N F Q R D P E      335
GTG ATG CGT GTG TCC AAC AAG ATG AGA TTC CTC CAA CTG AAC TTC CAG AGA GAC CCG GAA      1005

E I I W S M S P V V D G V V I P D D P L      355
GAG ATT ATC TGG TCC ATG AGC CCT GTG GTG GAT GGT GTG GTG ATC CCA GAT GAC CCT TTG      1065

```

Figure 1A

V	L	L	T	Q	G	K	V	S	S	V	P	Y	L	L	G	V	N	N	L	375
GTG	CTC	CTG	ACC	CAG	GGG	AAG	GTT	TCA	TCT	GTG	CCC	TAC	CTT	CTA	GGT	GTC	AAC	AAC	CTG	1125
E	F	N	W	L	L	P	Y	I	M	K	F	P	L	N	R	Q	A	M	R	395
GAA	TTC	AAT	TGG	CTC	TTG	CCT	TAT	ATC	ATG	AAG	TTC	CCG	CTA	AAC	CGG	CAG	GCG	ATG	AGA	1185
K	E	T	I	T	K	M	L	W	S	T	R	T	L	L	N	I	T	K	E	415
AAG	GAA	ACC	ATC	ACT	AAG	ATG	CTC	TGG	AGT	ACC	CGC	ACC	CTG	TTG	AAT	ATC	ACC	AAG	GAG	1245
Q	V	P	L	V	V	E	E	Y	L	D	N	V	N	E	H	D	W	K	M	435
CAG	GTA	CCA	CTT	GTG	GTG	GAG	GAG	TAC	CTG	GAC	AAT	GTC	AAT	GAG	CAT	GAC	TGG	AAG	ATG	1305
L	R	N	R	M	M	D	I	V	Q	D	A	T	F	V	Y	A	T	L	Q	455
CTA	CGA	AAC	CGT	ATG	ATG	GAC	ATA	GTT	CAA	GAT	GCC	ACT	TTC	GTG	TAT	GCC	ACA	CTG	CAG	1365
T	A	H	Y	H	R	D	A	G	L	P	V	Y	L	Y	E	F	E	H	H	475
ACT	GCT	CAC	TAC	CAC	CGA	GAT	GCC	GGC	CTC	CCT	GTC	TAC	CTG	TAT	GAA	TTT	GAG	CAC	CAC	1425
A	R	G	I	I	V	K	P	R	T	D	G	A	D	H	G	D	E	M	Y	495
GCT	CGT	GGA	ATA	ATC	GTC	AAA	CCC	CGC	ACT	GAT	GGG	GCA	GAC	CAT	GGG	GAT	GAG	ATG	TAC	1485
L	F	G	G	P	F	A	T	G	L	S	M	G	K	E	K	A	L	S		515
TTC	CTC	TTT	GGG	GGC	CCC	TTC	GCC	ACA	GGC	CTT	TCC	ATG	GGT	AAG	GAG	AAG	GCA	CTT	AGC	1545
Q	M	M	K	Y	W	A	N	F	A	R	T	G	N	P	N	D	G	N		535
CTC	CAG	ATG	ATG	AAA	TAC	TGG	GCC	AAC	TTT	GCC	CGC	ACA	GGA	AAC	CCC	AAT	GAT	GGG	AAT	1605
P	C	W	P	R	Y	N	K	D	E	K	Y	L	Q	L	D	F	T	T		555
CTG	CCC	TGC	TGG	CCA	CGC	TAC	AAC	AAG	GAT	GAA	AAG	TAC	CTG	CAG	CTG	GAT	TTT	ACC	ACA	1665
V	G	M	K	L	K	E	K	K	M	A	F	W	M	S	L	Y	Q	S		575
AGA	GTG	GCC	ATG	AAG	CTC	AAG	GAG	AAG	AAG	ATG	GCT	TTT	TGG	ATG	AGT	CTG	TAC	CAG	TCT	1725
R	P	E	K	Q	R	Q	F	*												585
AGA	AGA	CCT	GAG	AAG	CAG	AGG	CAA	TTC	TAA											1755

GGGTGGCTATGCAGGAAGGAGGCCAAGAGGGGTTTGCCCCACCATTCCAGGCCCTGGGGAGACTAGCCATGGACATACC

TGGGGACAAGAGTTCTACCCAAGGGCGAATTCGTTTAAACCTGCAGGACTAG

Figure 1B

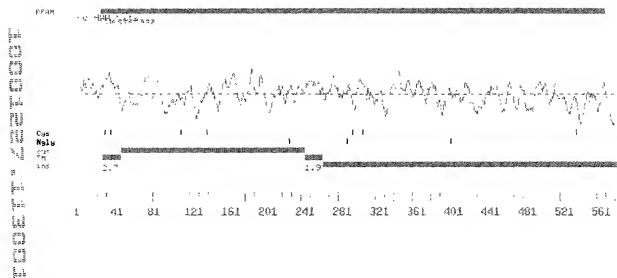


Figure 2

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM

hmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

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HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam5.5/Pfam

Sequence file: /prod/ddm/wspace/orfanal/oa-script.26660.seq

Query: 18903

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
COesterase	Carboxylesterases	558.6	4.1e-164	1

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
COesterase	1/1	25	569	1	612	558.6	4.1e-164

Alignments of top-scoring domains:

COesterase: domain 1 of 1, from 25 to 569: score 558.6, E = 4.1e-164

```

*->mvllllfLllllllliavlalaaakaspdp1lVatnnVlcGkvrGvnek
      +l+ +L 1 l ++ +l+a+++ ++ V t++ G+ G+
18903 25 RWILCWSLTLC1MAQTALGALHT---KRPQVVTKY---GTLQGKQMH 65

      tdngeqsvysFlGIPYAePPVGnLRFKaPqPYkepWsdvldAtkyppsCl
      + ++ +FlG+P+ PP+G LRF +P+P +epW++++dAt+ypP Cl
18903 66 VGKT--PIQVFLGVPPSRPPLGILRFAPPEP-PEPWGIRDATTYPGCL 112

      QdddfgfsldLKvalkmlslgwnklvg...lklSEDCLYLNvYtPknt
      Q + +g+ 1 +++ ++ + + 1 +sEDCLYLNvY P+ +
18903 113 Q-ESWGQ-----LASMYVSTRErykwLRFSEDCLYLNvYAPARA 150

      kpnslkPvMvWihGGGFmfGsghs1plslYdgeslaregnVivVsniYRL
      + + +lFvMvW +GG+F +G++ s+Y g+ la++++V++V ++ RL
18903 151 PGDPQLFvMvWfPGGAfIVGAA-----SSYEGSDLAAREKVVLFQHLR 195

      Gp1GFLstgddklpgsGnyGLIDQr1ALkVWqdNiaaFGGDPnsVTifGe
      G++GFLst+d+++ GN+GLIDQ +AL+VWq+NiaaFGGDP++VT+fG+
18903 196 GIFGFLSTDDSHAR--GNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGCL 243

      SAGaasVsl1ll1sngGDnppsskgLfhRAIsqSGsalspwa1qsesnarg
      SAGA+S+s 1++s P++ gLfhRAIsqSGS+al +i+s+ +
18903 244 SAGAMSISGLMMS-----FLA-SGLFhRAIsqSGTALFRlFTSNP--LK 285

      rakelar1lGcnetssselldCLRksaeLleatrsfllfeyvpflplf
      ak+aa 1-Gcnet+s 1+ CLR s + + + + +f+ f+
18903 286 VAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNK-MRFLQLNFRQDP 334

      1...aFgPvvdGdDapeafipedPeelikeCkfadvPyliGvtkdeEGgy
      ++ + +PvvdG+ +ip+dP+ 1+ +Gk + vPyl Gv++ E+ +
18903 335 Eei1wSMSFVVDGV-----VIPDDPLVLLTQGVSSVPYLLGVNNLEFNW 379

```

Figure 3A

```

faamllnasskgedelkktetnpdvlellkyllfyasealnikdMddlad
++++ +++ + + ket ++ l+ ll+ + + +
18903 380 LLPYIMKFPLNR-QAMRKETITK-MLWSTRRTLLN-ITKEQ-----VP 418

kvlekYpgdvddfsvesrknlgdmltDl1FkcptrvaadlhakhggsPv
v e+Y++ v + + ++ + d++ D +F+++ + ++ +++g Pv
18903 419 LVVEEYLDNVNEHDWKMLRNRMMDIVQDATFVYA-TLQTAHYHRDAGLPV 467

YaYvfdhpasfgigQflakrvdpefggavHgdEiffvFgnpllkeqlyka
Y+Y+f h+a+ + v+p+++ga+HgdE++f+Fg p+ ++ l
18903 468 YLYEFEHHAR-----GIIVKPRTDGADHGDEMYFLFGGPPATG-LS-- 507

teeeeksssktmmnywanFAktGnPnngtsnglvvWpkytseeqYslll
e+++s +mm+ywanFA+tGnP n++ +l+ Wp y+++e +l+
18903 508 MGKEKALS-LQMMKYWANFARTGNP-NDG--NLPCWPRYNKDEK--YLQL 551

llttitaqklkardprkvlcnfw<-*
+tt +klk+++ ++fw
18903 552 DFTTRVGMKLKEKK-----MAFW 569

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//
Searching for complete domains in SMART

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Figure 3B

GAP of: FrGcgManager_76_IOA8lnWg_ check: 5132 from: 1 to: 1983

Fbhl8903FL - Import - vector trimmed

to: FrGcgManager_76_JOA3WXZ1_ check: 1319 from: 1 to: 2456

Z34105 in Patent Nucleotide

Symbol comparison table: /ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/nwsgapdna.cmp
CompCheck: 8760

Gap Weight: 12 Average Match: 10.000
Length Weight: 4 Average Mismatch: 0.000

Quality: 13796 Length: 2746
Ratio: 6.957 Gaps: 14
Percent Similarity: 92.617 Percent Identity: 92.617

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

FrGcgManager_76_IOA8lnWg_ x FrGcgManager_76_JOA3WXZ1_

COE-2 1CCT 3

Z34105 101 CATTTGCGCTTGCTGACGGCGTCGAGCCCTGGCCAGACATGTCCACAGGG 150

4 TTAGCCAATTTCGGCCGAGGCCCTCCCGCCOCAGTA.CTTGCTGGCAGGGAT 52

|| || | ||| | | |||| | || | || ||

151 TTCCTCCTTCGGGTCGGGACTCTGGGCTCCACCACCGTGGCCCGCCGGCGG 200

53 TAAGAGCAGA.TAAAAGTGTGCTCACACACTGTAGACACGGCTACCATGC 101

| |||| | || |||| | | || |||| |

201 GACCAGCAGACGGCGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAACC 250

102 CATC.....CACAGTGTGGCATCCACAGTGTGGCATCACTCCTGC. 143

|| | || | || | | | | |||| |

251 CTTCTGTGGGCTCAATTTTGGAATCTTGGAAGTACTTCAACTCCAGCA 300

144 .CCACAGCAGGAGCT..GGCTGGAGCATGAGGTGGATTCTGTG..CTGGA 188

| ||| | | || ||| || || || || |

301 ACTACATCTGCTCCTTCAAGTGGTTTGGGAACCGGGCTCTTTGGATCTAA 350

Figure 4A

766 GGTGCAGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCC 815
 |||
 1050 GGTGCAGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCC 1099
 |||
 816 TGTTCGGCCAGTCGGCGGGGCCATGAGCATCTCAGGACTGATGATGTCA 865
 |||
 1100 TGTTCGGCCAGTCGGCGGGGCCATGAGCATCTCAGGACTGATGATGTCA 1149
 |||
 866 CCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCAGAGTGGCACCGC 915
 |||
 1150 CCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCAGAGTGGCACCGC 1199
 |||
 916 GTTATTTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAAGAAG 965
 |||
 1200 GTTATTTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAAGAAG 1249
 |||
 966 TTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAAC 1015
 |||
 1250 TTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAAC 1299
 |||
 1016 TGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGAT 1065
 |||
 1300 TGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGAT 1349
 |||
 1066 GAGATTCCTCCAACCTGAACCTCCAGAGAGACCCGGAAGAGATTATCTGGT 1115
 |||
 1350 GAGATTCCTCCAACCTGAACCTCCAGAGAGACCCGGAAGAGATTATCTGGT 1399
 |||
 1116 CCATGAGCCCTGTGGTGGATGGTGTGGTGATCCAGATGACCCCTTGGTG 1165
 |||
 1400 CCATGAGCCCTGTGGTGGATGGTGTGGTGATCCAGATGACCCCTTGGTG 1449
 |||
 1166 CTCCTGACCCAGGGGAAGTTTCATCTGTGCCCTACCTTCTAGGTGTCAA 1215
 |||
 1450 CTCCTGACCCAGGGGAAGTTTCATCTGTGCCCTACCTTCTAGGTGTCAA 1499
 |||
 1216 CAACCTGGAATTCAAATGGCTCTTGCCCTTATATCATGAAGTTCCCGCTAA 1265
 |||
 1500 CAACCTGGAATTCAAATGGCTCTTGCCCTTAT 1530
 .
 1316 CGCACCTGTTGAATATACCAAGGAGCAGGTACCACCTGTGGTGGAGGA 1365
 |||
 1531AATATACCAAGGAGCAGGTACCACCTGTGGTGGAGGA 1568
 |||
 1366 GTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTA 1415
 |||
 1569 GTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTA 1618
 |||

Figure 4C

1416 TGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACT 1465
 |||
 1619 TGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACT 1668
 |||
 1466 GCTCACTACCACCGAGATGCCGGCCTCCTGTCTACCTGTATGAATTGA 1515
 |||
 1669 GCTCACTACCACCGA..... 1683
 .
 1666 CAACTTTGCCCGCACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGGC 1715
 |||
 1684GAAACCCCAATGATGGGAATCTGCCCTGCTGGC 1716
 .
 1716 CACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGA 1765
 |||
 1717 CACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGA 1766
 .
 1766 GTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTGGATGAGTCTGTA 1815
 |||
 1767 GTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTGGATGAGTCTGTA 1816
 .
 1816 CCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCA 1865
 |||
 1817 CCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCA 1866
 .
 1866 GGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGAC 1915
 |||
 1867 GGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGAC 1916
 .
 1916 TAGCCATGGACATACCTGGGGACAAGAGTTCTACCCCAAGGGCAATTCGT 1965
 |||
 1917 TAGCCATGGACATACCTGGGGACAAGAGTTCTACCCA...CCCA...GT 1960
 .
 1966 TTAAACCTGCAGGA.CTAG..... 1983
 |||
 1961 TTAGAATGCAGGAGCTCCTGCTGCCTCCAGGCCAAAGCTAGAGCTTTT 2010
 .

Figure 4D

ALIGN calculates a global alignment of two sequences
 version 2.0 Please cite: Myers and Miller, CABIOS (1989)
 COE-2 584 aa vs.
 PRO873 545 aa
 scoring matrix: BLOSUM50, gap penalties: -12/-2
 62.4% identity; Global alignment score: 2271

```

                                10
COE-2  M-----PST-----VLPSTVLPSSLPTAG
      :               :.  :.  :.  :.
PRO873 MSTGFSFGSGTLGSTTTVAAGGTSTGGVFSFGTGTSSNPNVGLNFGNLGSTSTPATTSAPS
      10         20         30         40         50         60

      20         30         40         50         60         70
COE-2  AGWSMRWILCWSLTLCMAQTALGALHTKRPQVVTKYGTLLQGGQMHVGTKPIQVFLGVFP
      :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
PRO873 SGFGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLLQGGQMHVGTKPIQVFLGVFP
      70         80         90        100        110        120

      80        90        100        110
COE-2  SRPPLGILRFAPPEPPEPWKGIRDATTYPG-----
      :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
PRO873 SRPPLGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASL
      130        140        150        160        170        180

                                120        130        140        150
COE-2  -----CLQESWGLASMYVSTRERYKWLRFSEDCLYLNVIYAPARAPGDPQLPVM
      :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
PRO873 LPQPLSVWGYRCLQESWGLASMYVSTRERYKWLRFSEDCLYLNVIYAPARAPGDPQLPVM
      190        200        210        220        230        240

      160        170        180        190        200        210
COE-2  VWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMA
      :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
PRO873 VWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMA
      250        260        270        280        290        300

      220        230        240        250        260        270
COE-2  ALRWVQENIAAFGGDPGNVTLFGQSAGAMISGLMMSPLASGLFHRAISQSQTALFRLFI
      :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
PRO873 ALRWVQENIAAFGGDPGNVTLFGQSAGAMISGLMMSPLASGLFHRAISQSQTALFRLFI
      310        320        330        340        350        360

      280        290        300        310        320        330
COE-2  TSNPLKVAKKVAHLAGCNHNSTQILVNCILRALSGTKVMRVSNKMRFLQLNLFQRPDEEIIW
      :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
PRO873 TSNPLKVAKKVAHLAGCNHNSTQILVNCILRALSGTKVMRVSNKMRFLQLNLFQRPDEEIIW
      370        380        390        400        410        420

```

Figure 5A

```

      340      350      360      370      380      390
COE-2  SMSPVVDGVVIPDDPLVLLTQGVSSVPYLLGVNNLEFNWLLPYIMKFPINRQAMRKETI
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
PRO873 SMSPVVDGVVIPDDPLVLLTQGVSSVPYLLGVNNLEFNWLLPY-----
      430      440      450      460

      400      410      420      430      440      450
COE-2  TKMLWSTRLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMDIVQDATFVYATLQTAHY
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
PRO873 -----NITKEQVPLVVEEYLDNVNEHDWKMLRNRMDIVQDATFVYATLQTAHY
      470      480      490      500      510

      460      470      480      490      500      510
COE-2  HRDAGLPVYLYEFEHHARGIIVKPRTDGADHGDEMYFLFGGPFATGLSMGKEKALSQMM
      ::.. :.. : : : :
PRO873 HRET--PMM-----GIC--P---AGHA-----
      520

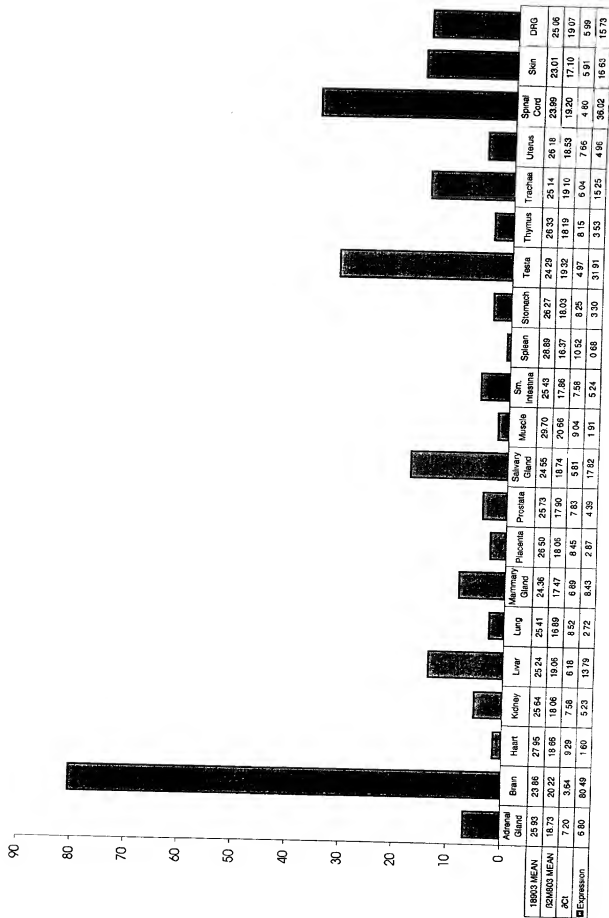
      520      530      540      550      560      570
COE-2  KYWANFARTGNPNNDGNLPCWPRYNKDEKYLQLDFTTRVGMKLEKKMAFWMSLYQSRPE
      : : : : : : :
PRO873 -----TTRM-----KSTCSWIL-----P-
      530      540

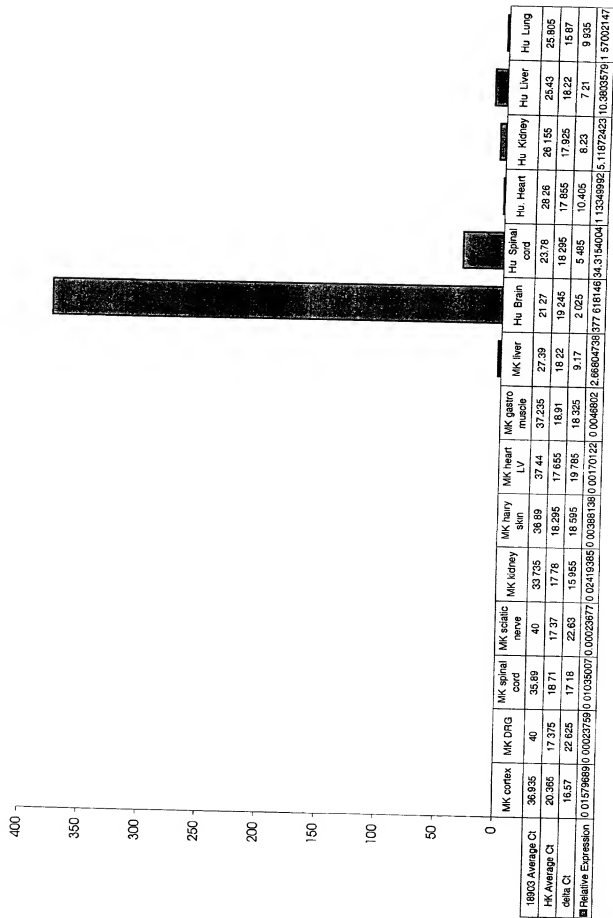
      580
COE-2  KQRQF
      :
PRO873 -QEWA

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Figure 5B

Figure 6





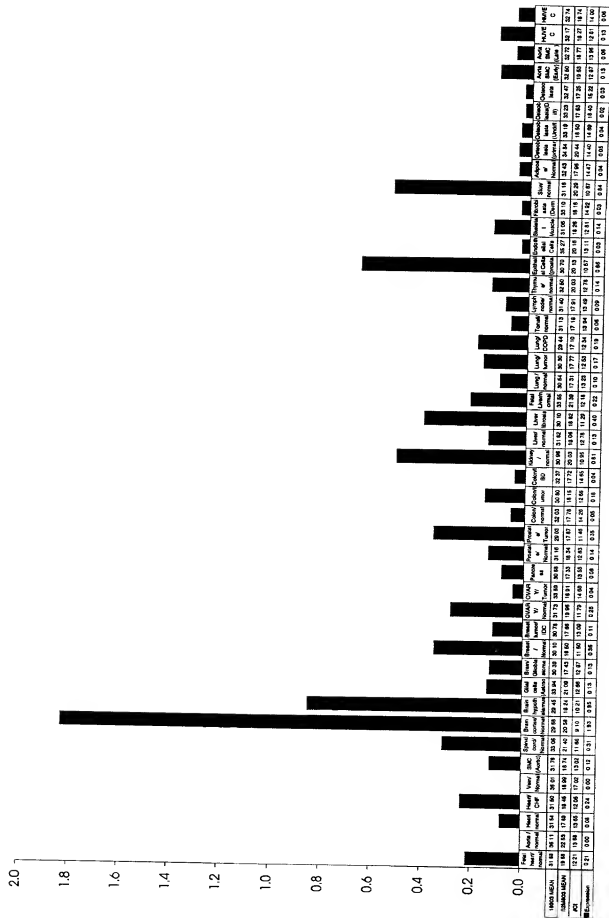
[illegible]

Figure 8B

Tissue	18903 MEAN	62M803 MEAN	•Ct	Expression
Fetal heart/ normal	31.89	19.68	12.21	0.21
Aorta / normal	36.11	22.53	13.58	0.00
Heart normal	31.54	17.89	13.65	0.08
Heart/ CHF	31.50	19.45	12.05	0.24
Vein/ Normal	36.01	18.99	17.02	0.00
SMC (Aortic)	31.76	18.74	13.02	0.12
Spinal cord/ Normal	33.06	21.40	11.66	0.31
Brain cortex/ Normal	29.68	20.58	9.10	1.83
Brain hypothalamus/ Normal	29.45	19.24	10.21	0.85
Glial cells (Astrocytes)	33.94	21.09	12.86	0.13
Brain/ Glioblastoma	30.39	17.43	12.97	0.13
Breast/ Normal	30.10	18.60	11.50	0.35
Breast/ Tumor/ IDC	30.75	17.66	13.09	0.11
Ovary/ Normal	31.73	19.95	11.79	0.28
Ovary/ Tumor	33.59	18.91	14.68	0.04
Pancreas	30.88	17.33	13.55	0.08
Prostate/ Normal	31.16	18.34	12.83	0.14
Prostate/ Tumor	29.03	17.57	11.46	0.35
Colon/ normal	32.03	17.78	14.26	0.05
Colon/ tumor	30.80	18.15	12.66	0.16
Colon/IBD	32.37	17.72	14.65	0.04
Kidney/ normal	30.98	20.03	10.95	0.51
Liver/ normal	31.82	19.08	12.75	0.15
Liver fibrosis	30.10	18.82	11.29	0.40
Fetal Liver/normal	33.55	21.39	12.16	0.22
Lung / normal	30.54	17.31	13.23	0.10
Lung/ tumor	30.30	17.77	12.53	0.17
Lung/ COPD	29.44	17.10	12.34	0.19
Tonsil/ normal	31.13	17.19	13.94	0.06
Lymph node/ normal	31.40	17.91	13.49	0.09
Thymus/ normal	32.80	20.03	12.78	0.14
Epithelial Cells (prostate)	30.70	20.13	10.57	0.66
Endothelial Cells (aortic)	35.27	20.16	15.11	0.03
Skeletal Muscle/ Normal	31.06	18.26	12.81	0.14
Fibroblasts (Dermal)	33.10	18.18	14.92	0.03
Skin/ normal	31.16	20.29	10.87	0.54
Adipose/ Normal	32.43	17.96	14.47	0.04
Osteoblasts (primary)	34.84	20.44	14.40	0.05
Osteoblasts (Undiff)	33.19	18.50	14.69	0.04
Osteoblasts(Diff)	33.23	17.83	15.40	0.02
Osteoclasts	32.47	17.25	15.22	0.03
Aorta SMC (Early)	32.50	19.53	12.97	0.13
Aorta SMC (Late)	32.72	18.77	13.96	0.06
HUVEC	32.17	19.27	12.91	0.13
HMVEC	32.74	18.74	14.00	0.06

40.00 40.00 0.00